

CLEAN VERSION OF REWRITTEN AND ADDED PARAGRAPHS

PURSUANT TO 37 CFR § 1.21 (b)(1)(ii)

IN THE SPECIFICATION:

Please insert the following paragraph in the specification:

~~Insert~~ the following language as the first paragraph in that portion of the specification relating to the "Description Of The Figures" (Page 12, Before line 15).

--The file of this patent contains at least one drawing executed in color. Copies of this patent with color drawing(s) will be provided by the Patent and Trademark Office upon request and payment of necessary fees.--

The following amendment is offered to harmonize the reference to highlighted elements in a Formal Drawing (e.g. Figure 1) with the description of this same Figure in the Specification.

~~Please replace the paragraph beginning at page 12, line 15, and ending on page 12, line 24, with the following rewritten paragraph:~~

✓ --Figure 1 shows the nucleotide sequence (SEQ ID NO:1) of the λ73 cDNA and the deduced primary structure of Pet-1 (SEQ ID NO:2). The two sets of numbering on the right mark either the nucleotide sequence or amino acid residues. Translation termination codons flanking the open reading frame are marked by asterisks. The ETS domain is contained within the dashed lines. Underlined amino-acid sequences within the ETS domain mark homologous region in other ETS-domains that were used to prepare primers for the degenerate PCR screen. Boxed residues indicate putative MAP kinase phosphorylation sites. A putative nucleotide binding P-loop is enclosed by an oval. A possible polyadenylation signal motif is shown in capital letters at the end of the nucleotide sequence.--

The following amendment is offered to harmonize the reference to highlighted elements in a Formal Drawing (e.g. Figure 2A) with the description of this same Figure in the Specification.

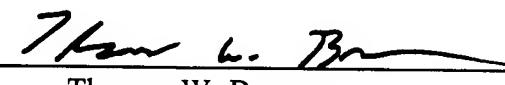
A Please replace the paragraph beginning at page 12, line 25, and ending on page 13, line 5, with the following rewritten paragraph:

-- Figure 2 show the alignment of various ETS-domain sequences. A) The first three letters of each ETS-domain factor designation shown on the left indicate an organism, e.g. DRO, *Drosophila melanogaster*, followed by the common gene name. Columns of more than 40% sequence identity are in bold text. B) Parsimony analysis of sequences encoding different ETS domains. The phylogenetic tree demonstrates relative similarities among the ETS DNA binding domains of Pet-1, Ets-1 and members of the ERG subfamily. The available sequence for the Drosophila ETS-3 ETS domain is incomplete (Chen, T., *et al.*, "Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain" *Dev. Biol.* 151:176-191, 1992). Branch lengths do not represent estimates of evolutionary distances between protein sequences.--

CONCLUSION

This amendment to the Specification does not introduce new matter and will not require an additional search of the prior art by the Examiner. Therefore, the Applicants respectfully request the examiner to make it of record in the instant application. Should the Examiner have any additional questions or comments, the Applicants encourage the Examiner to call the undersigned collect at (617) 252-3353.

Dated: April 12, 2002


Thomas W. Brown
Registration No. 50,002

MEDLEN & CARROLL, LLP
101 Howard Street, Suite 350
San Francisco, California 94105